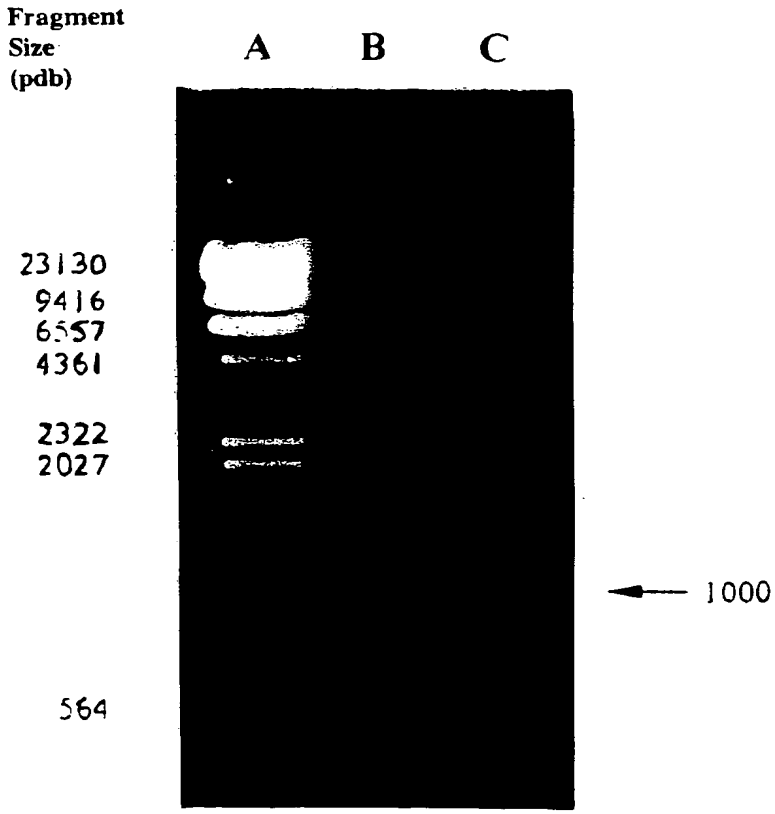

FIG. 1

FIG. 2A

HsKin-mmKin pep 16 10 1997 16 00

```
                     10         20         30         40         50         60         70         80         90        100
hsKin17.pep  MGKSDFLTPK AIANRIKSKG LQKLRWYCQM CQKQCRDENG FKCHCMSESH QRQLLLASEN PQQFMDYFSE EFRNDFLELL RRRFGTKRVH NNIVYNEYIS
                    *
mmKin17.pep  MGKSDFLSPK AIANRIKSKG LQKLRWYCQM CQKQCRDENG FKCHCMSESH QRQLLLASEN PQQFMDYFSE EFRNDFLELL RRRFGTKRVH NNIVYNEYIS
                    110        120        130        140        150        160        170        180        190        200
hsKin17.pep  HREHIHMNAT QWETLTDFTK WLGREGLCKV DETPKGWYIQ YIDRDPETIR RQLELEKKKK QDLDDEEKTA KFIEEQVRRG LEGKEQEVPT FTELSRENDE
                                                                                                            * *         *
mmKin17.pep  HREHIHMNAT QWETLTDFTK WLGREGLCKV DETPKGWYIQ YIDRDPETIR RQLELEKKKK QDLDDEEKTA KFIEEQVRRG LEGKEQETPV FTELSRENEE
                    210        220        230        240        250        260        270        280        290        300
hsKin17.pep  EKVTFNLSKG ACSSSGATSS KSSTLGPSAL KTIGSSASVK RKESSQSSTQ SKEKKKKKSA LDEIMEIEEE KKRTARTDYW LQPEIIVKII TKKLGEKYHK
                    *    ** *   *     *        **  *  *          ** ****             *            *     * *
mmKin17.pep  EKVTFNLNKG AGGSAGATTS KSSSLGPSAL KLLGSAASGK RKESSQSS   AQPAKKKKSA LDEIMELEEE KKRTARTDAW LQPGIVVKII TKKLGEKYHK
                    310        320        330        340        350        360        370        380        390        400
hsKin17.pep  KKAIVKEVID KYTAVVKMID SGDKLKLDQT HLETVIPAPG KRILVLNGGY RGNEGTLESI NEKTFSATIV IETGPLKGRR VEGIQYEDIS KLA
               **       *       *     *                    *                      *
mmKin17.pep  KKGVVKEVID RYTAVVKMTD SGDRLKLDQT HLETVIPAPG KRVLVLNGGY RGNEGTLESI NEKAFSATIV IETGPLKGRR VEGIQYEDIS KLA
                    410        420        430        440        450        460        470        480        490        500
hsKin17.pep
             <==
mmKin17.pep  <==
```

FIG. 2B

hsKin17-mmKin17 16 10 1997 15 59

```
                    10        20        30        40        50        60        70        80        90       100
hsKin17 . seq       TGATTCGAGC TCGGTACCCG GGGATCCGAT TAGAAAGTGA TCGCTGCCGT GGTCGCCATG GGGAAGTCGG ATTTTCTTAC TCCCAAGGCT ATCGCCAACA
                                                                          *                 * * *     *           *
mmKin17 . seq                                                             ATG GGCAAGTCGG ATTTTCTGAG CCCCAAGGCT ATCGCCAATA
                   110       120       130       140       150       160       170       180       190       200
hsKin17 . seq       GGATCAAGTC CAAGGGGCTG CAGAAGCTAC GCTGGTATTG CCAGATGTGC CAGAAGCAGT GCCGGGACGA GAATGGCTTT AAGTGTCATT GTATGTCCGA
                    * *       *  *     *        *                 * *   *                       *           *
mmKin17 . seq       GAATTAAGTC CAAAGGGCTC CAGAAGCTTC GCTGGTACTG CCAGATGTGC CAAAAGCAAT GCCGCGACGA GAATGGCTTT AAGTGTCACT GTATGTCTGA
                   210       220       230       240       250       260       270       280       290       300
hsKin17 . seq       ATCTCATCAG AGACAACTAT TGCTGGCTTC AGAAAATCCT CAGCAGTTTA TGGATTATTT TTCAGAGGAA TTCCGAAATG ACTTTCTAGA ACTTCTCAGG
                      *       *         *                                                                 *         *
mmKin17 . seq       ATCTCATCAA AGACAACTGT TGCTGGCTTC AGAAAACCCT CAGCAGTTTA TGGATTATTT TTCAGAGGAA TTCCGAAATG ACTTTCTGGA ACTTCTGAGG
                   310       320       330       340       350       360       370       380       390       400
hsKin17 . seq       AGACGCTTTG GCACTAAAAG GGTCCACAAC AACATTGTCT ACAACGAATA CATCAGCCAC CGAGAGCACA TCCACATGAA TGCCACTCAG TGGGAAACTC
                    *                                                   *                             * * *       * *
mmKin17 . seq       CGACGCTTTG GCACTAAAAG GGTCCACAAC AACATTGTCT ACAATGAATA CATCAGCCAC CGAGAGCACA TCCACATGAA CGCTACCCAG TGGGAGACAC
                   410       420       430       440       450       460       470       480       490       500
hsKin17 . seq       TGACTGATTT TACTAAGTGG CTGGGCAGAG AAGGCTTGTG CAAAGTGGAC GAGACACCAA AAGGCTGGTA TATTCAGTAC ATAGACAGGG ACCCAGAAAC
                     * *     *                 *       *     *       *           *                 *
mmKin17 . seq       TGACCGACTT TACCAAGTGG CTGGGCAGAG AGGGCTTGTG TAAAGTGGAT GAGACACCGA AAGGCTGGTA CATTCAGTAC ATAGACAGAG ACCCAGAAAC
```

FIG. 2C

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                   510        520        530        540        550        560        570        580        590        600
hsKin17.seq  TATCCGCCGG CAACTGGAAC TGGAGAAAAA GAAAAAGCAG GACCTTGATG ATGAAGAAAA AACTGCCAAA TTTATTGAAG AGCAAGTGAG AAGAGGCCTG
             *     *             *  *  *         *     *   *  *  *                      *   *     *      *
mmKin17.seq  CATCCGTCGG CAACTGGAAT TAGAAAAAAA GAAGAAGCAA GATCTGGACG ATGAAGAAAA AACTGCCAAG TTCATTGAGG AGCAGGTGAG AAGAGGCCTG
                   610        620        630        640        650        660        670        680        690        700
hsKin17.seq  GAAGGGAAGG AACAGGAGGT CCCTACTTTT ACGGAATTAA GCAGAGAAAA TGATGAAGAG AAAGTCACGT TTAATTTGAG TAAAGGAGCA TGTAGCTCAT
                     *   *      ** *   **       *   * *    *           *     *      *      *   *   *          * *  *     *
mmKin17.seq  GAAGGGAAAG AGCAGGAGAC ACCTGTTTTT ACAGAACTTA GCCGAGAAAA TGAGGAAGAA AAAGTTACGT TCAATCTGAA TAAAGGAGCG GGTGGCTCAG
                   710        720        730        740        750        760        770        780        790        800
hsKin17.seq  CCGGAGCAAC ATCTTCCAAG TCAAGTACTC TGGGACCGAG TGCACTGAAG ACGATAGGAA GTTCAGCATC AGTGAAACGA AAAGAATCTT CCCAGAGCTC
              *     *    * *            **  *        *              **   *  *   **        * *      *      *      *
mmKin17.seq  CGGGAGCTAC AACATCCAAG TCAAGCTCTT TGGGACCAAG TGCACTGAAG CTGCTGGGGA GCGCAGCATC CGGGAAACGG AAAGAGTCTT CACAGAGCTC
```

FIG. 2D

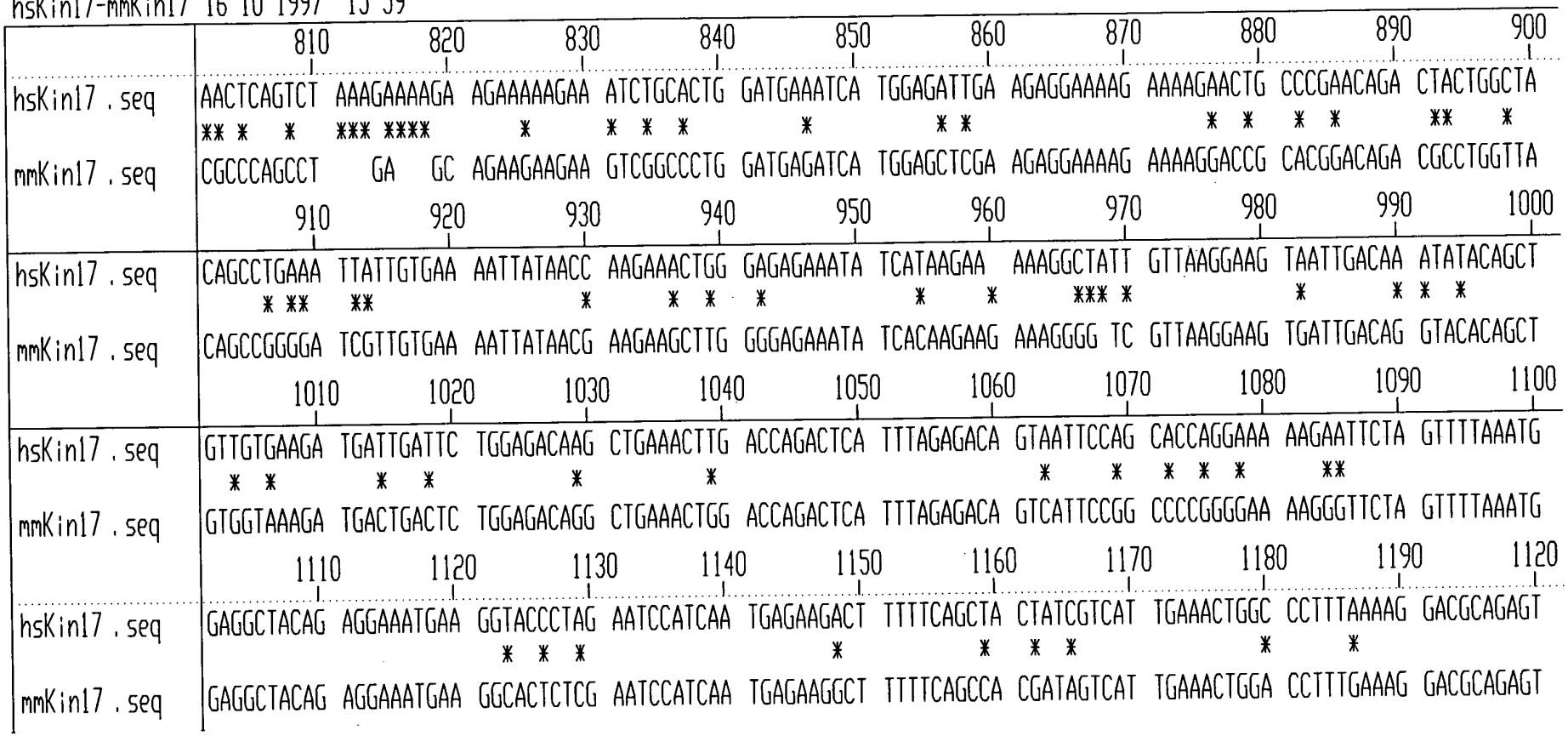


FIG. 2E

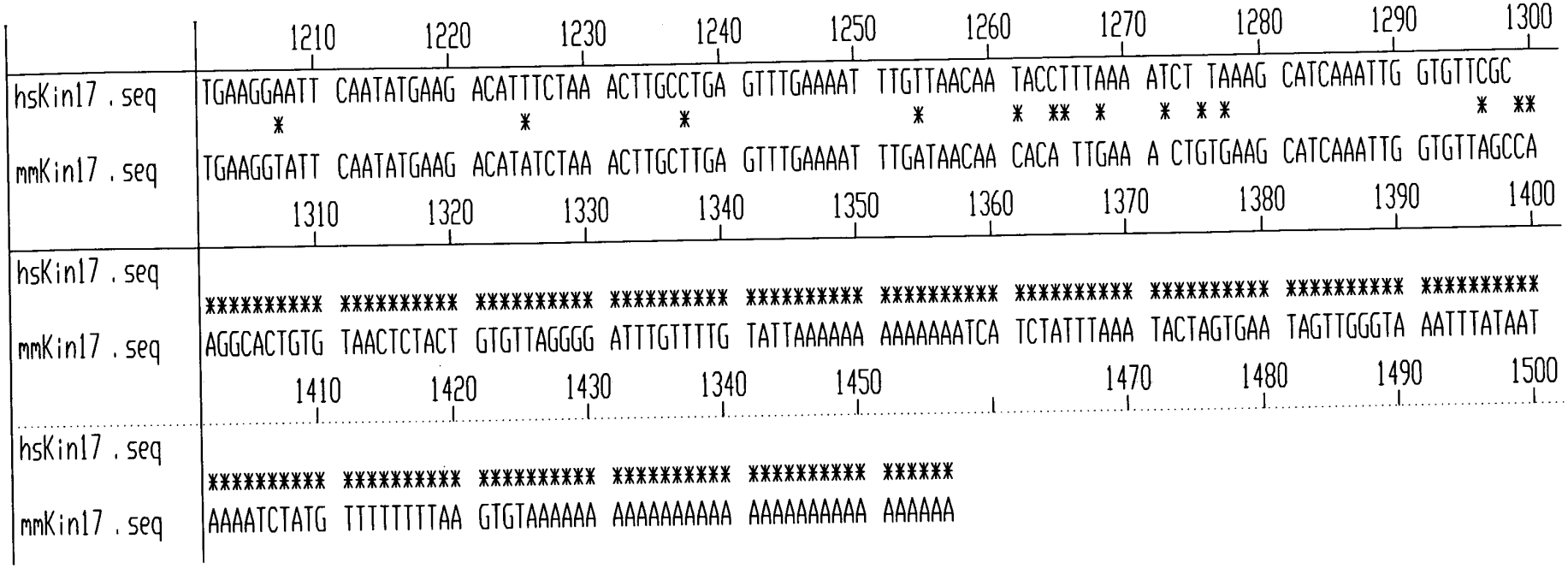


FIG. 3A

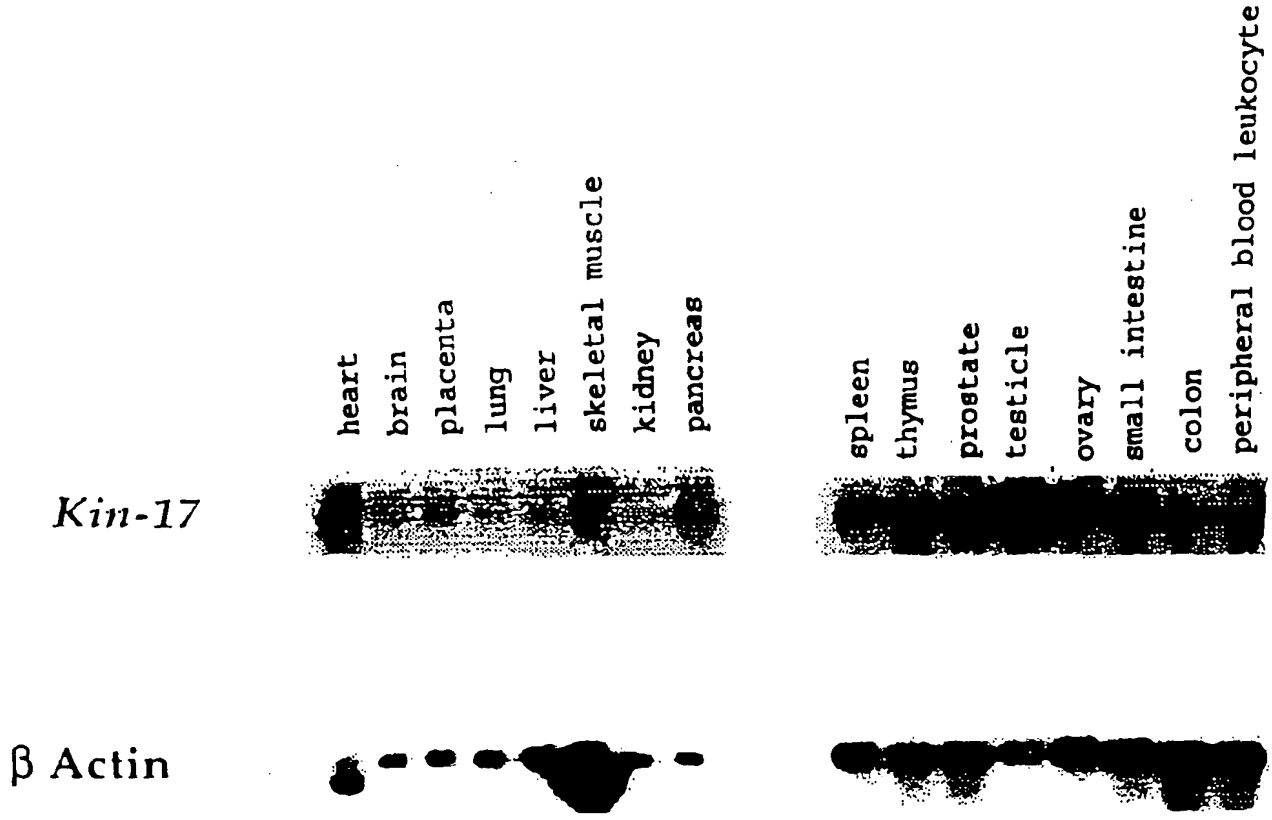


FIG. 3B

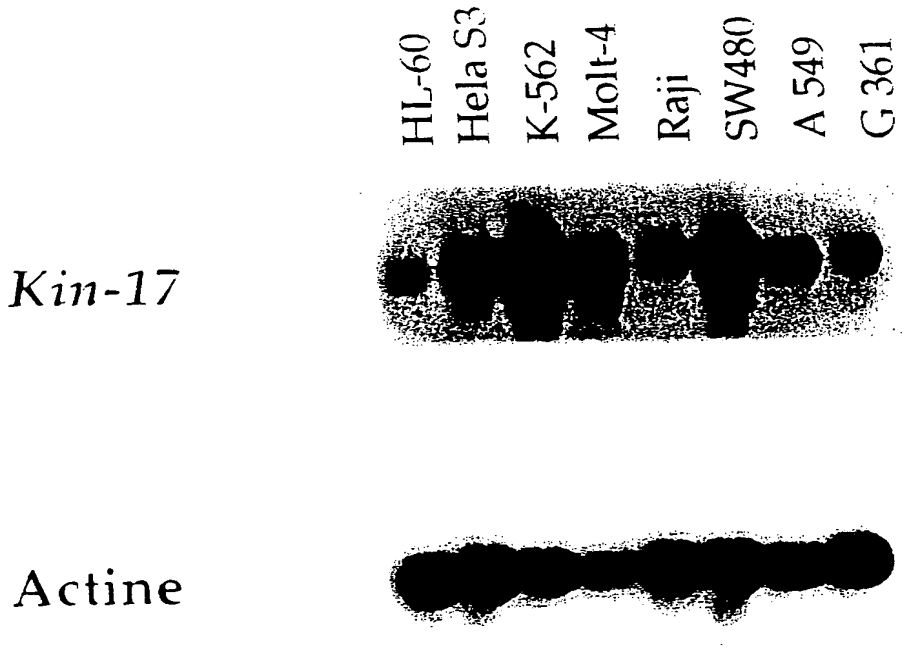


FIG. 4A

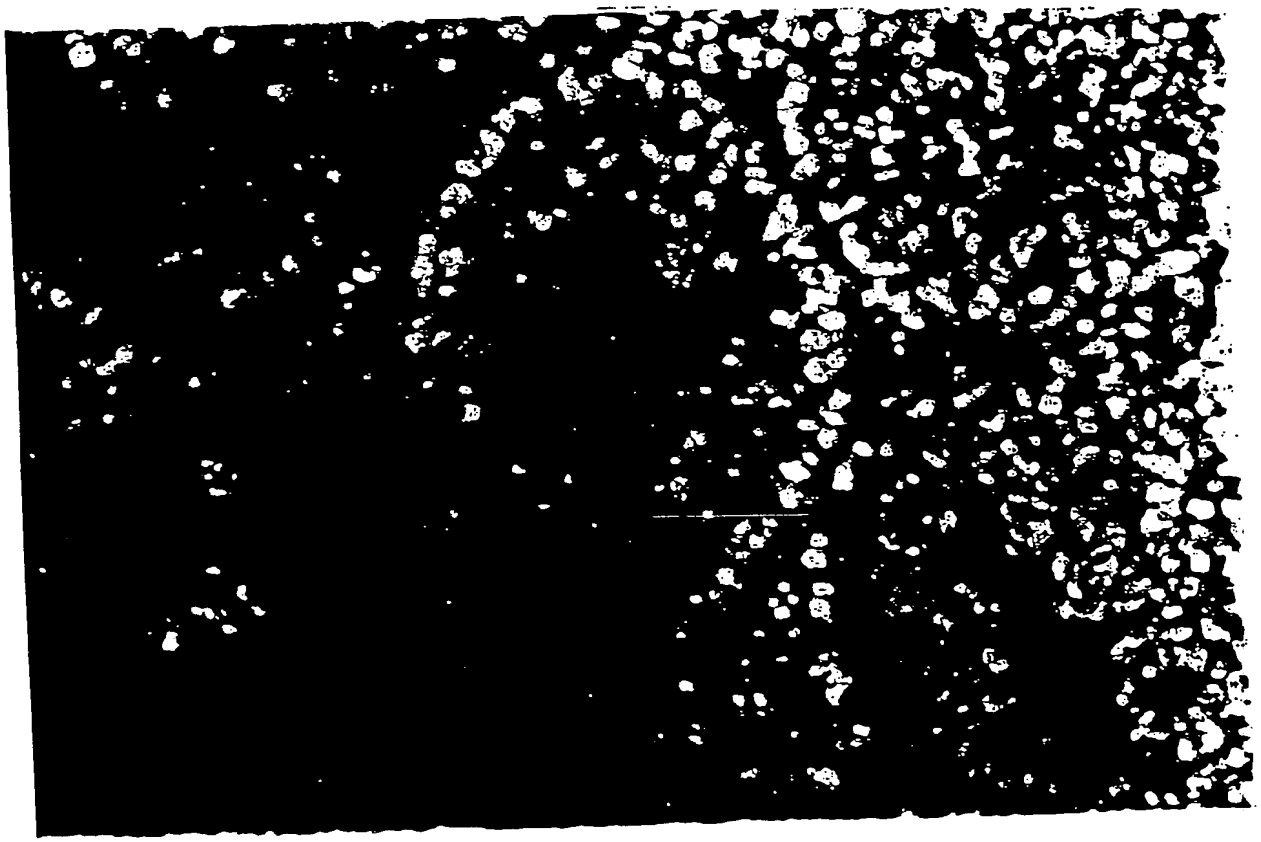


FIG. 4B

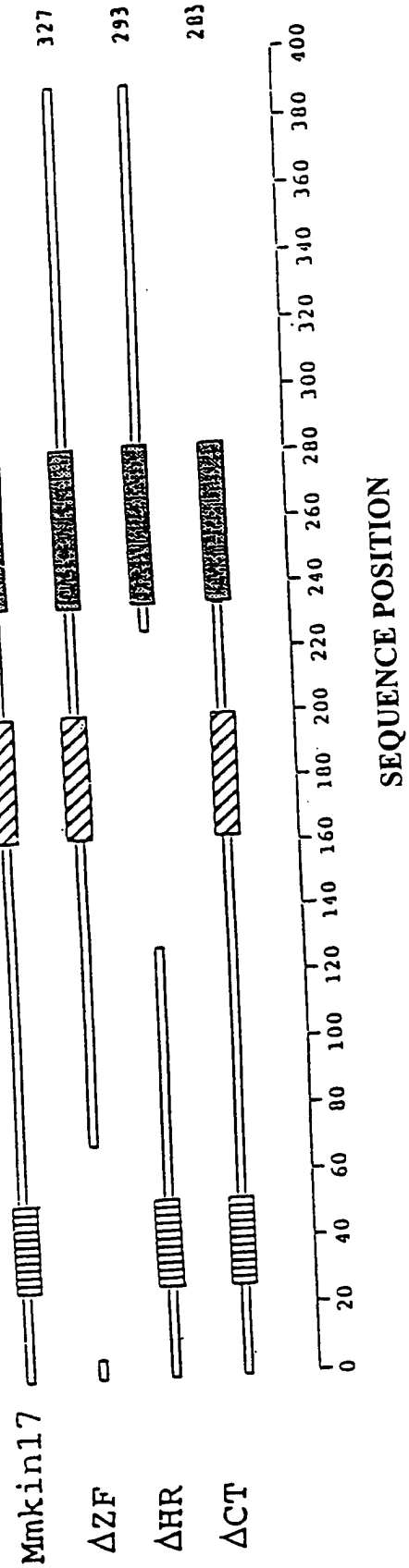


FIG. 5

FIG. 6A

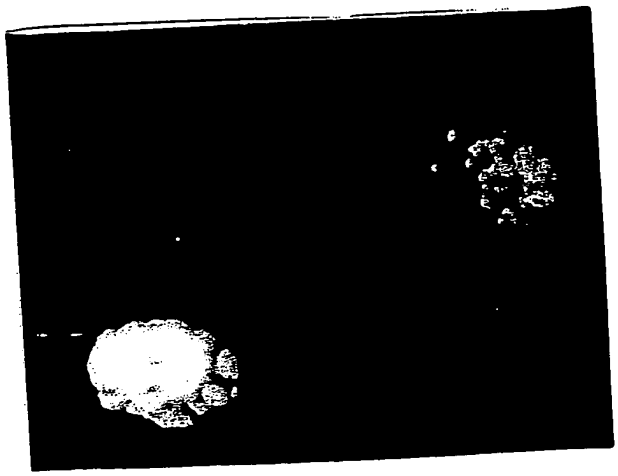


FIG. 6B

FIG. 7A

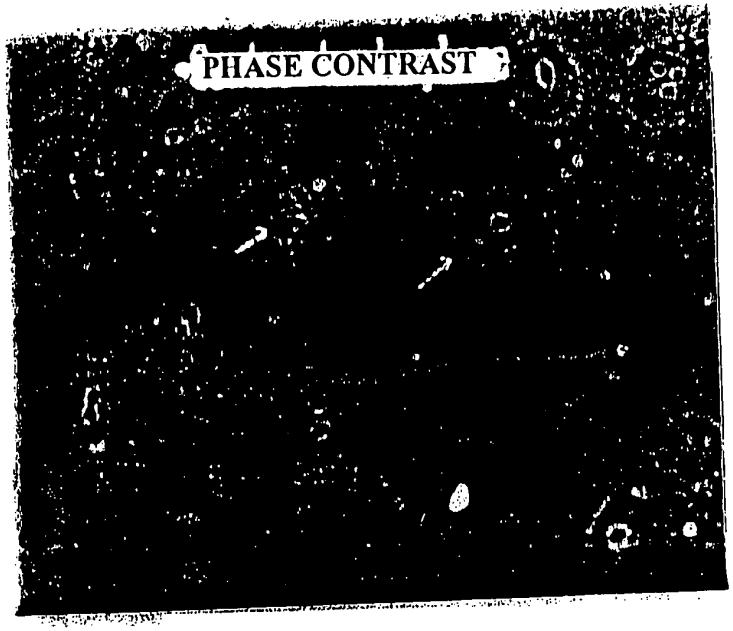


FIG. 7B

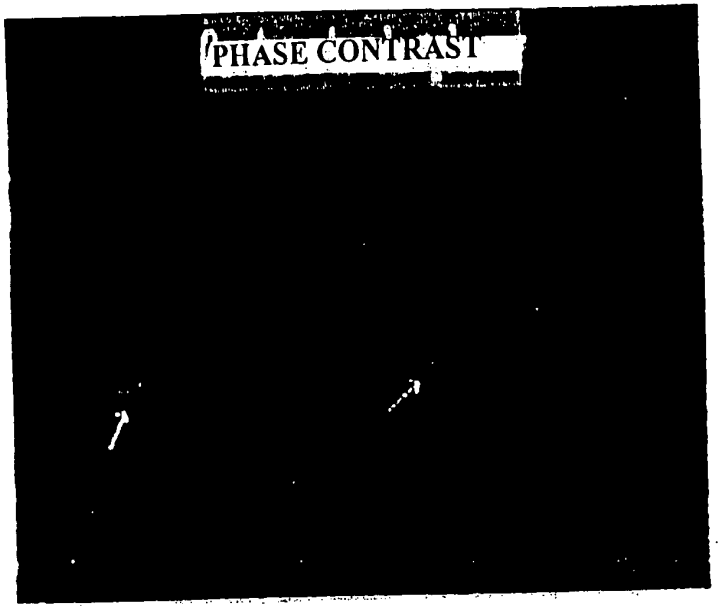


FIG. 8A

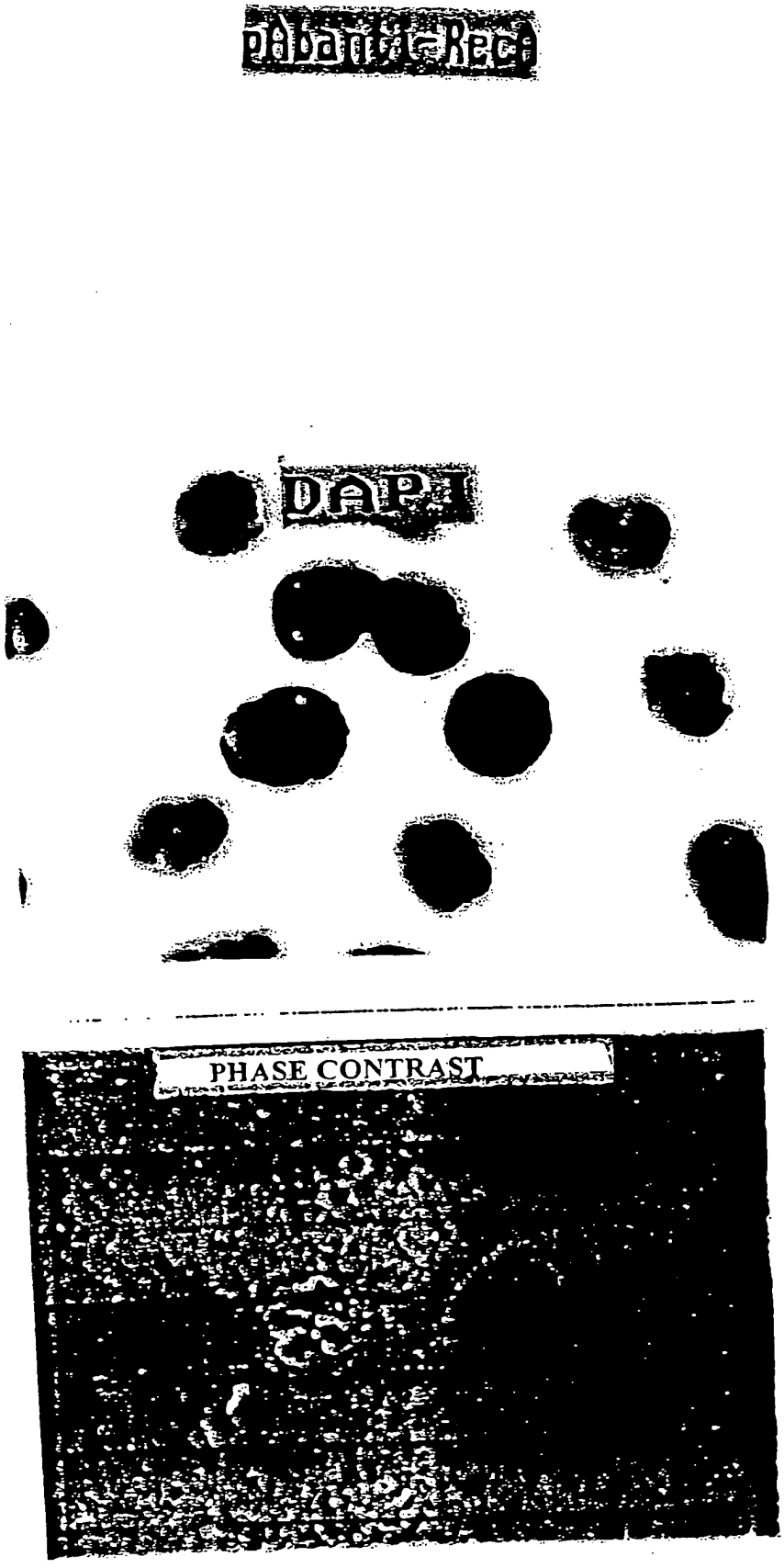
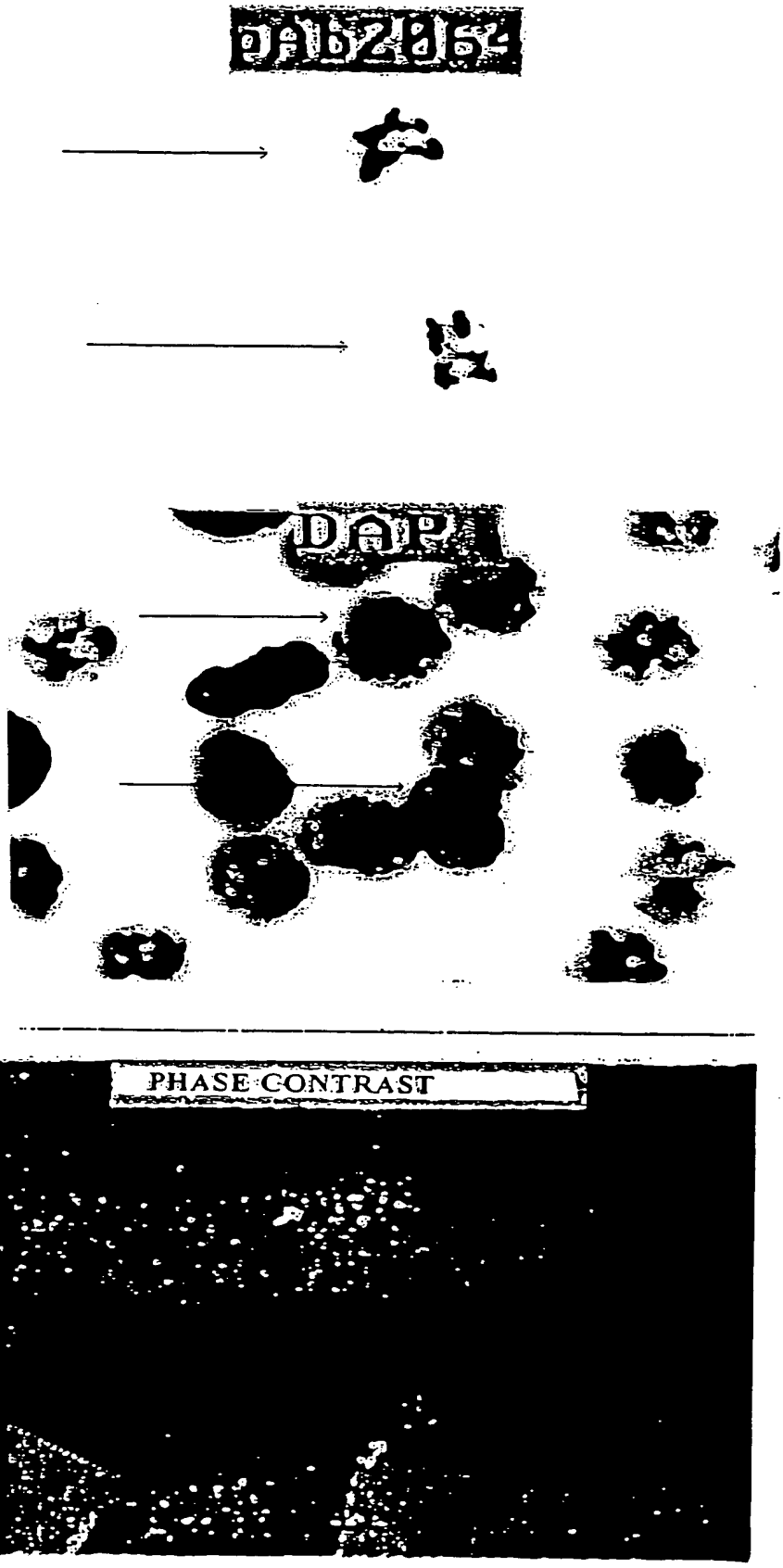


FIG. 8B



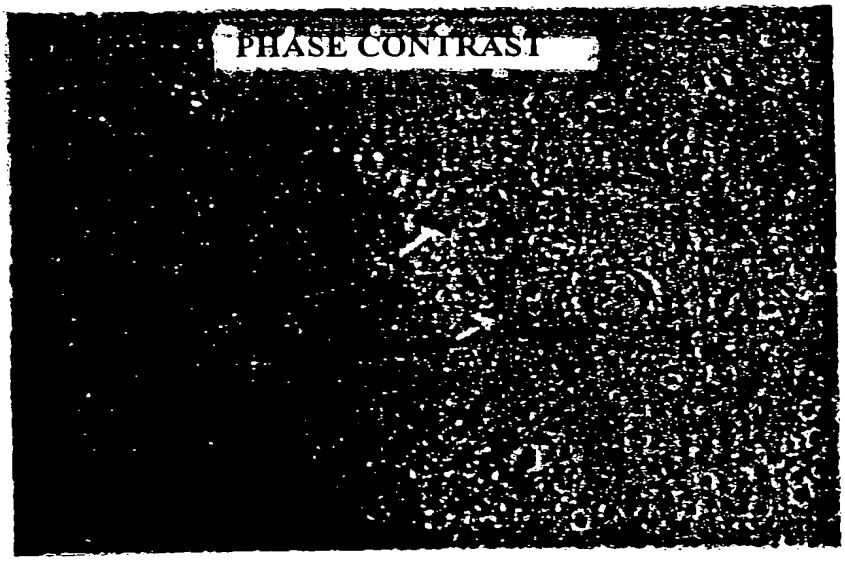


FIG. 9

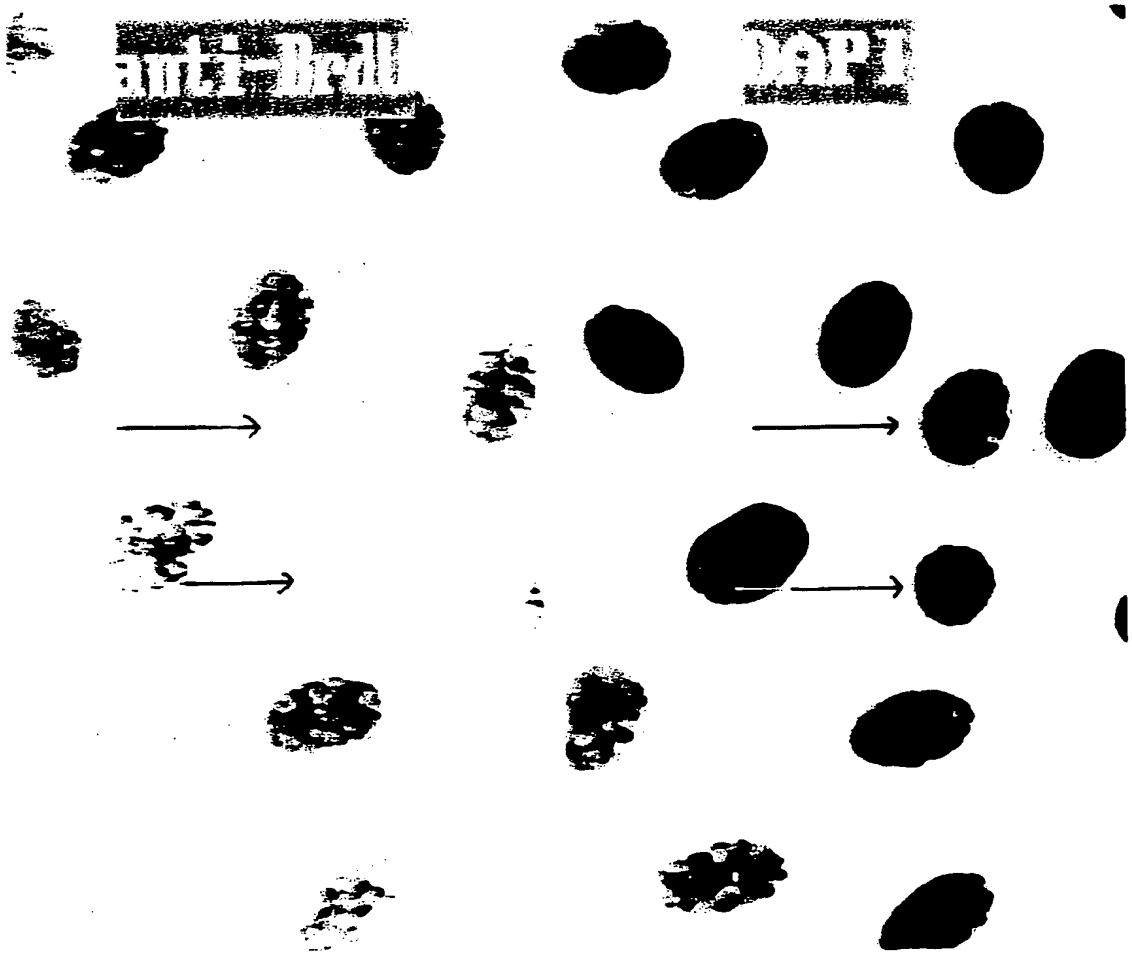
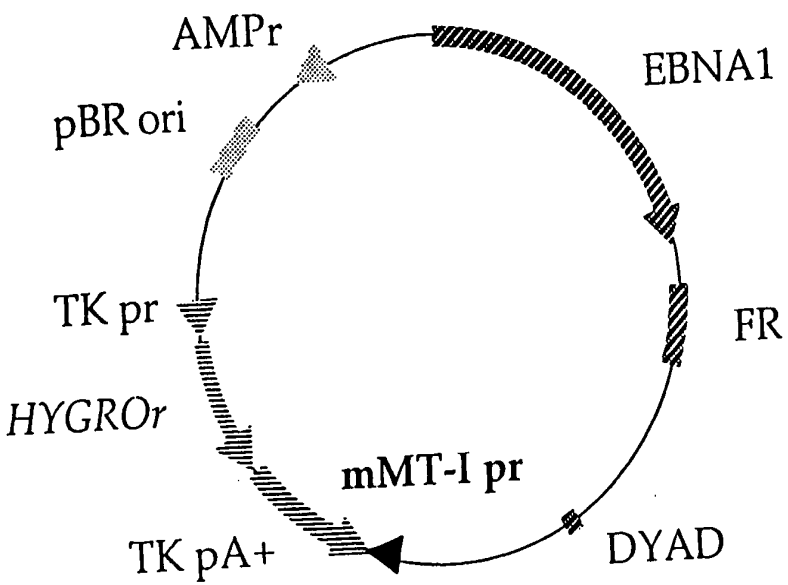


FIG. 10A

PROTEIN EXPRESSED	NONE	kin17		kinΔHR	kinΔCT
		LOW LEVEL	HIGH LEVEL		
% of Cells REPLICATING THEIR DNA	40	40	0	0	33

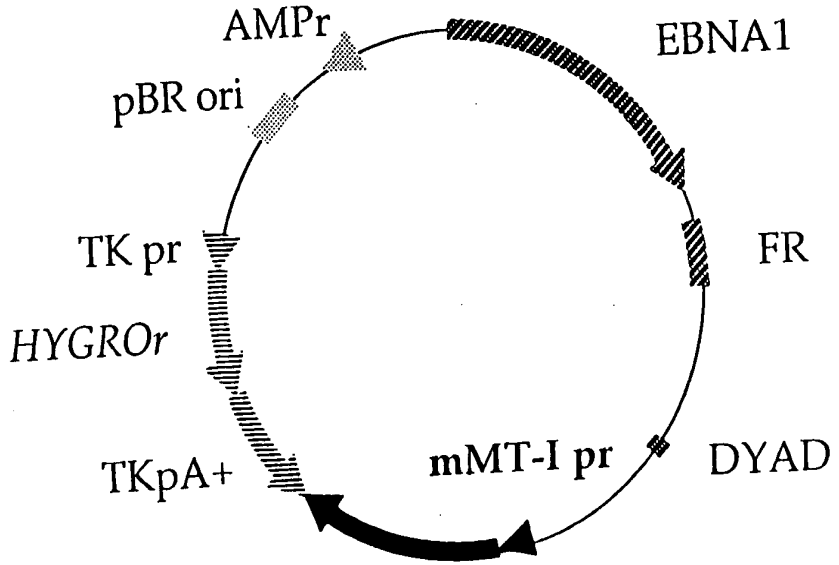
FIG. 10B



pEBVMTΔ (pB220)

(8824 bp)

FIG. 11A



$_{Mm}$Kin-17

pEBVMT$_{Mm}$Kin17 (pB223)

(10271 bp)

FIG. 11B

FIG. 12A

FIG. 12B

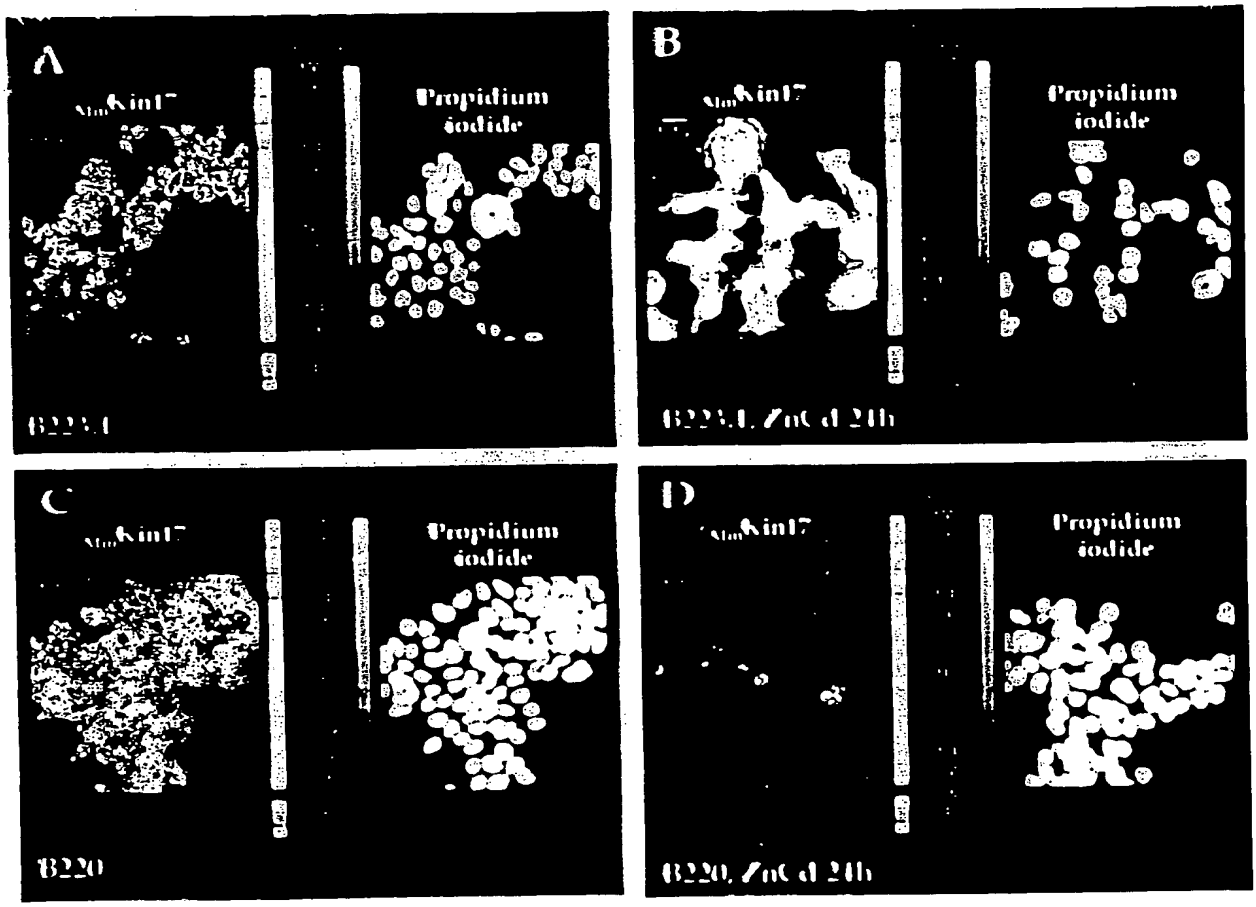


FIG. 12C

FIG. 12D

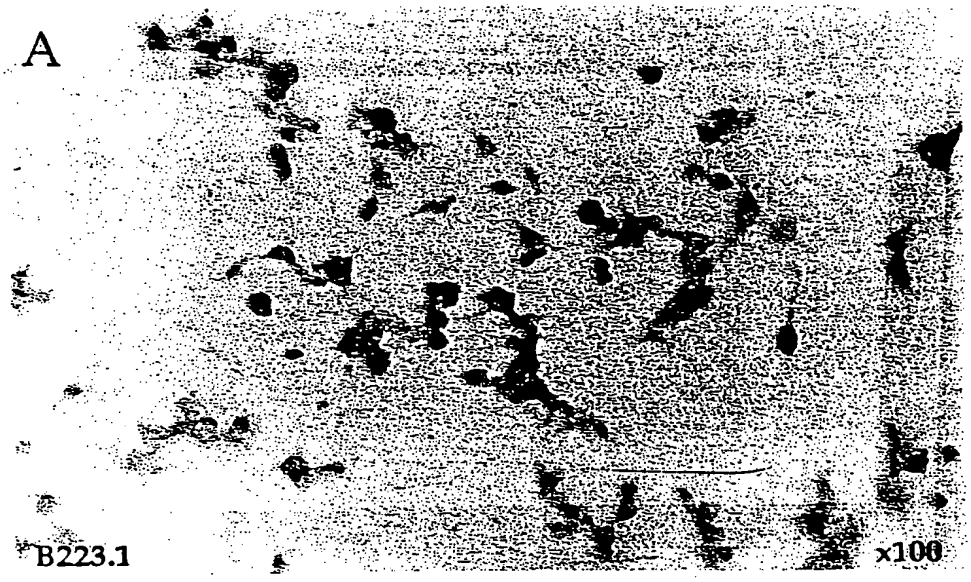


FIG. 13A

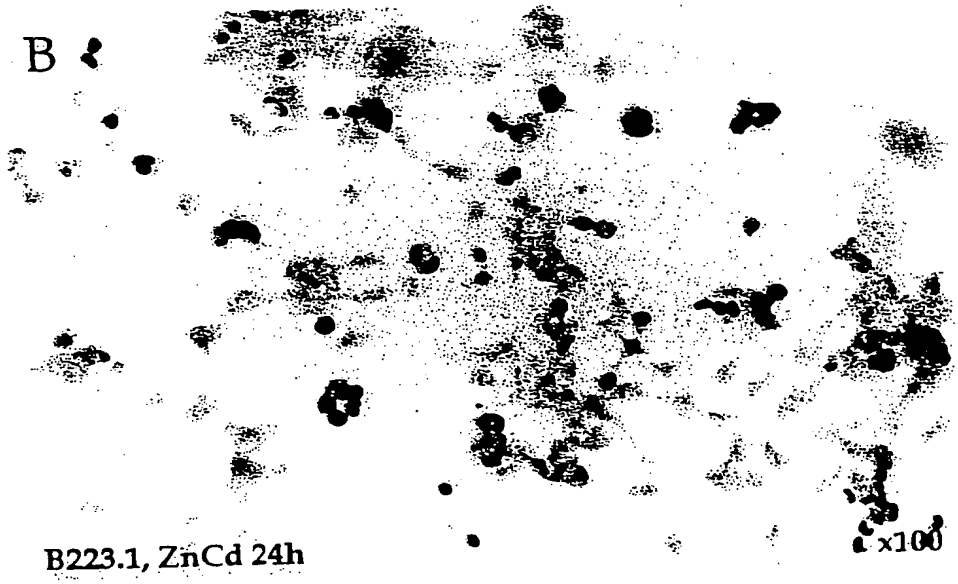


FIG. 13B

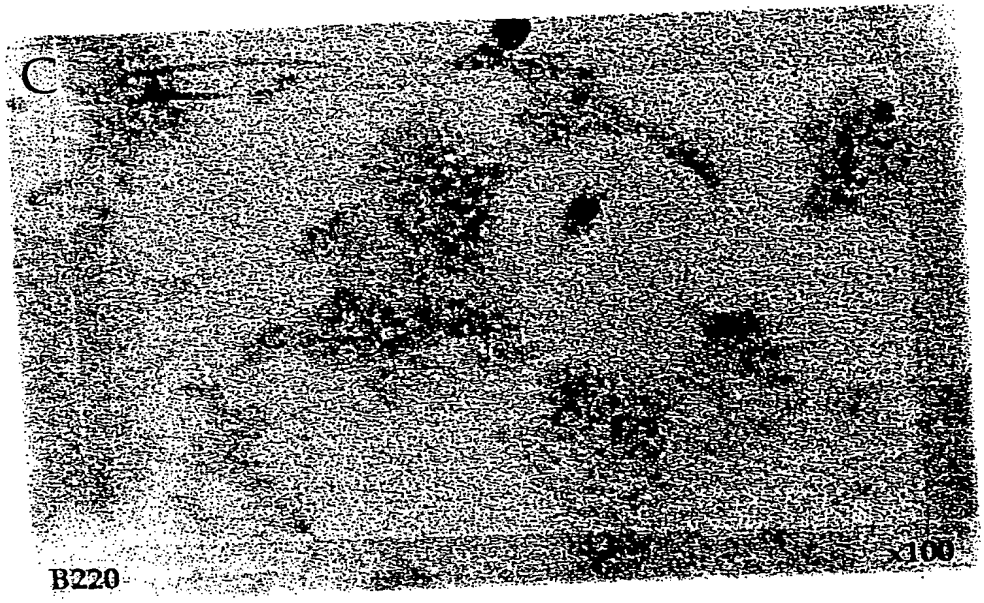


FIG. 13C

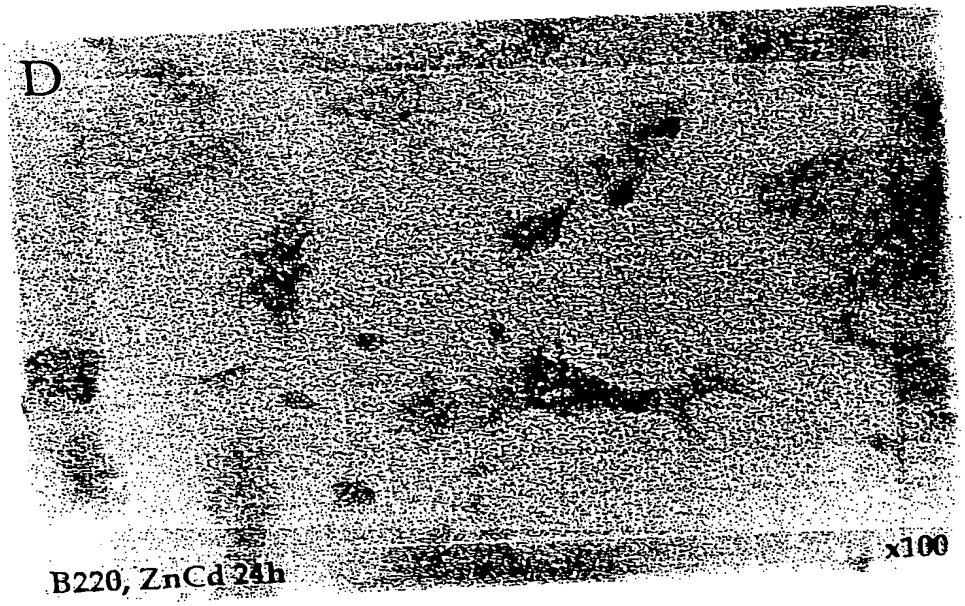


FIG. 13D

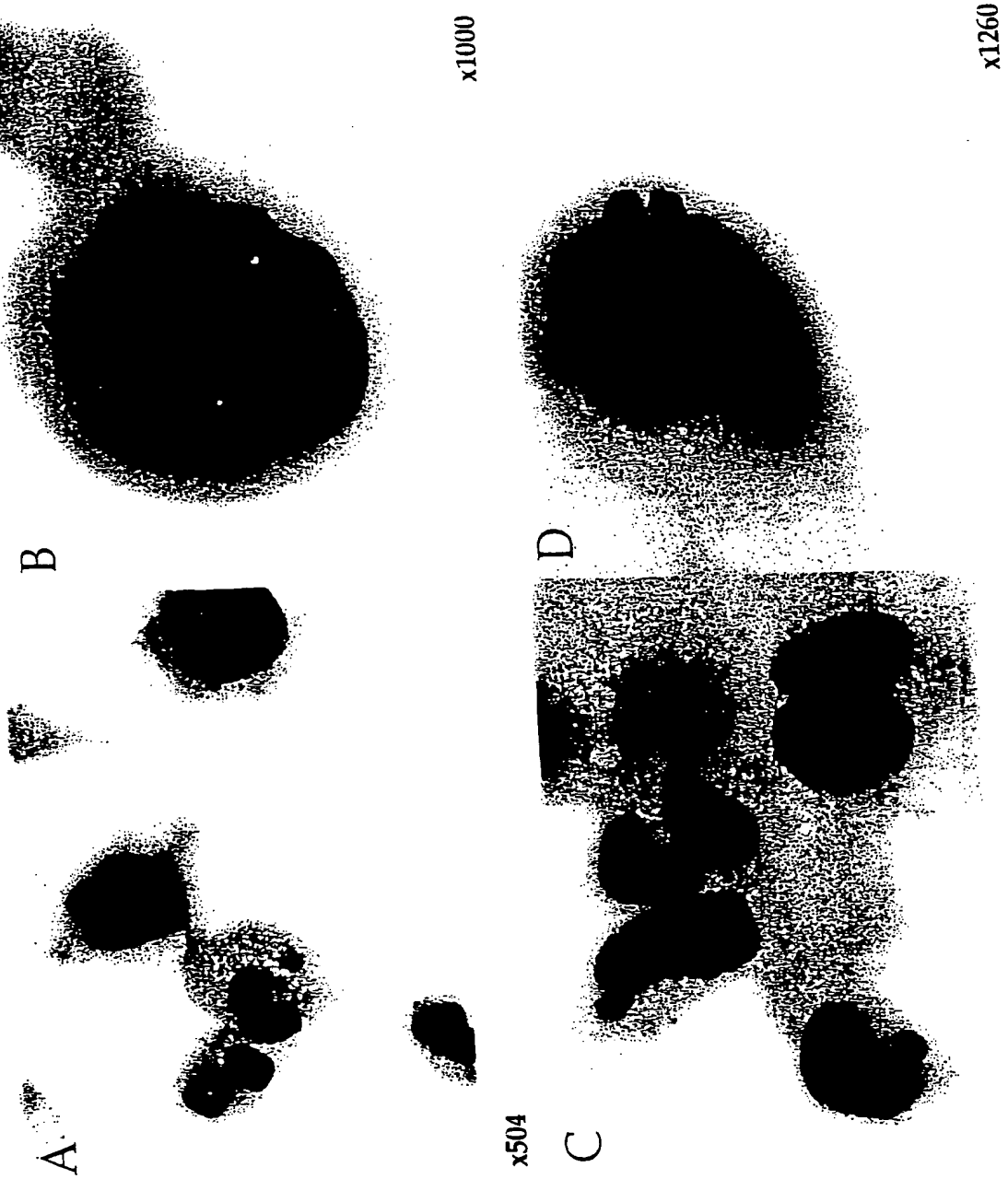
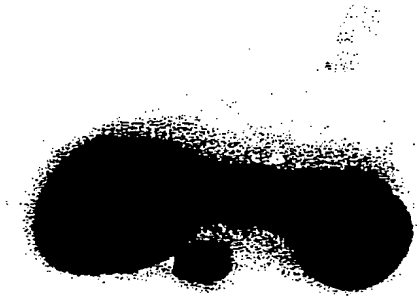


FIG. 14A

FIG. 14B

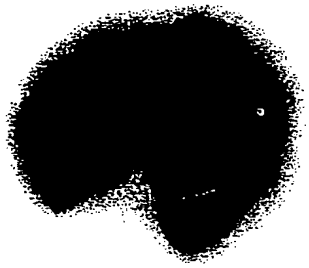
FIG. 14C

FIG. 14D



F x1260

FIG. 14F



E x2000

FIG. 14E

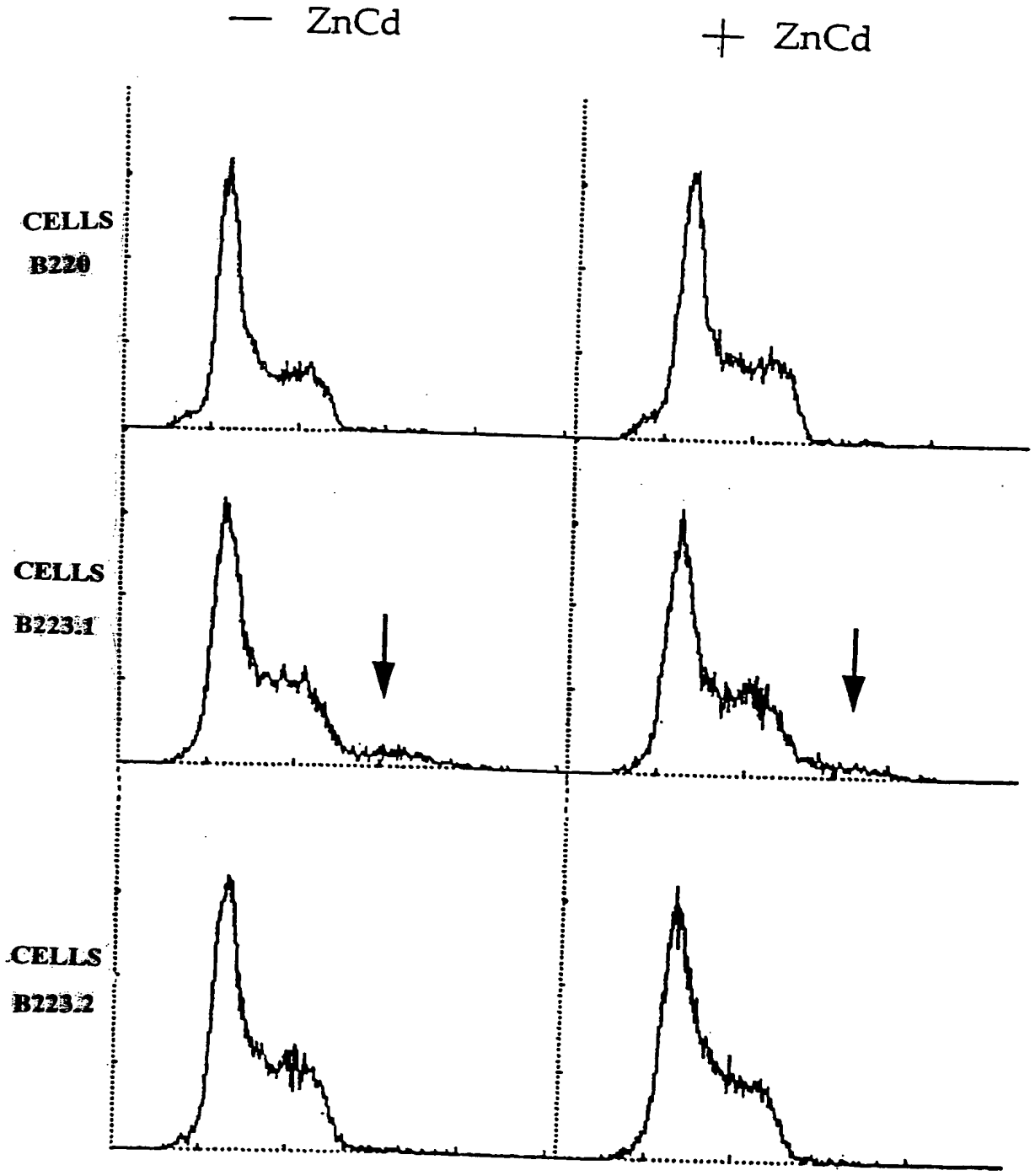


FIG. 15

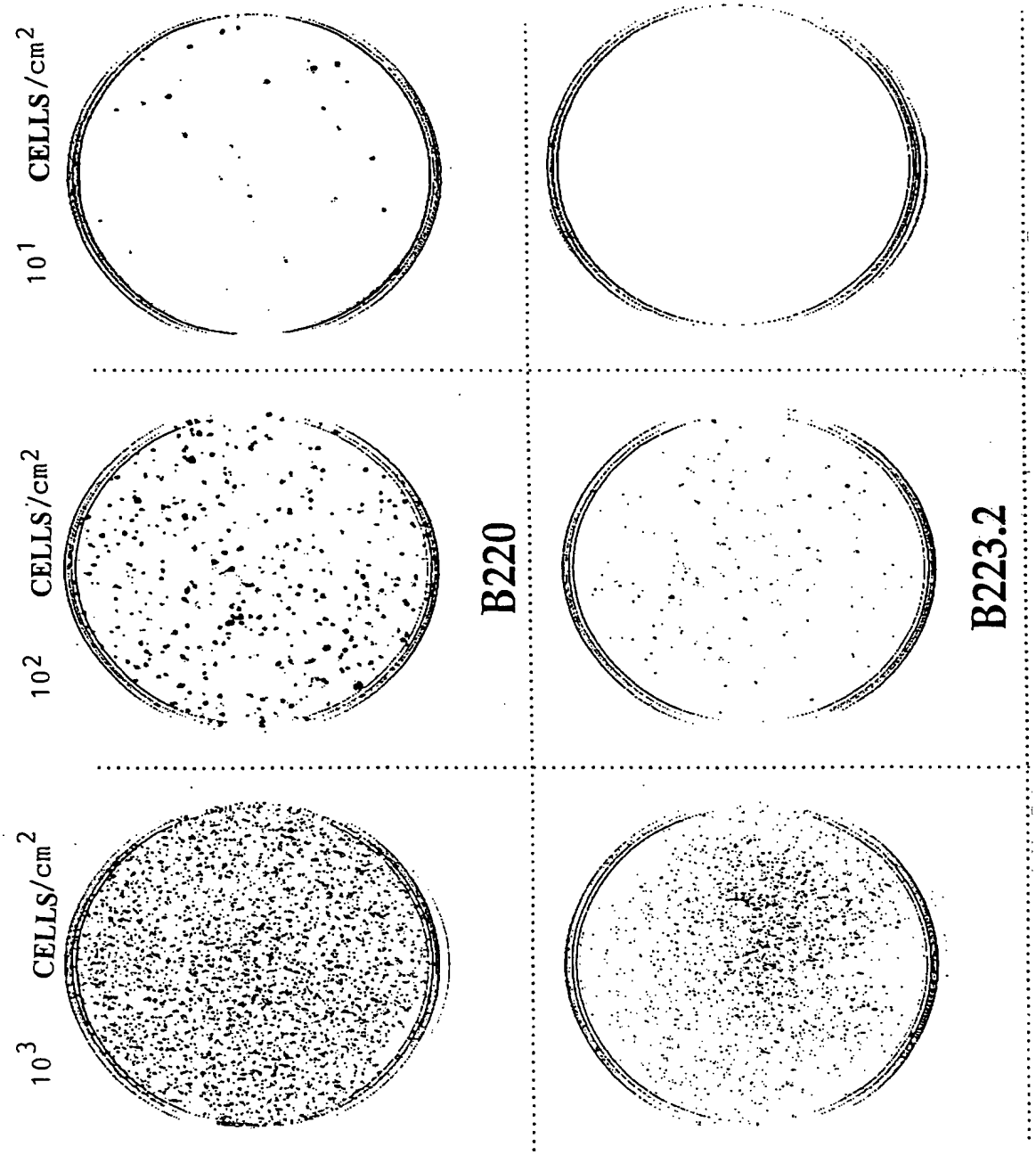


FIG. 16A

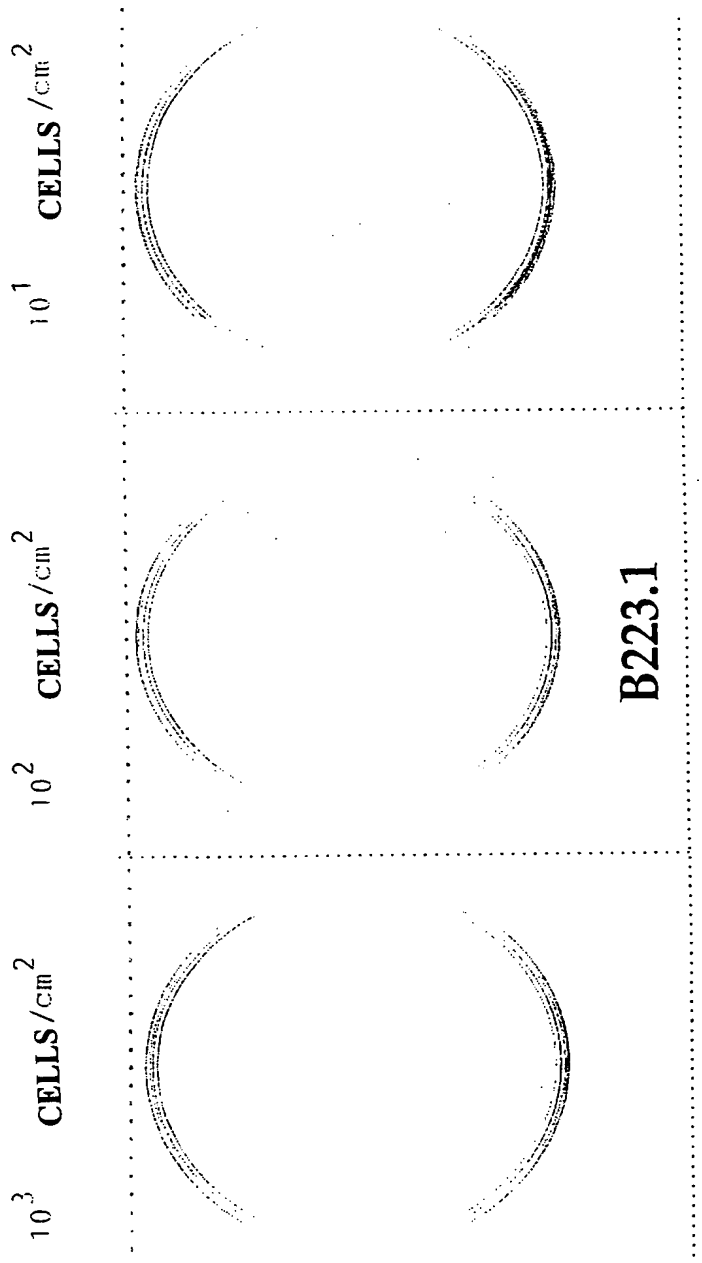


FIG. 16B

FIG. 17A

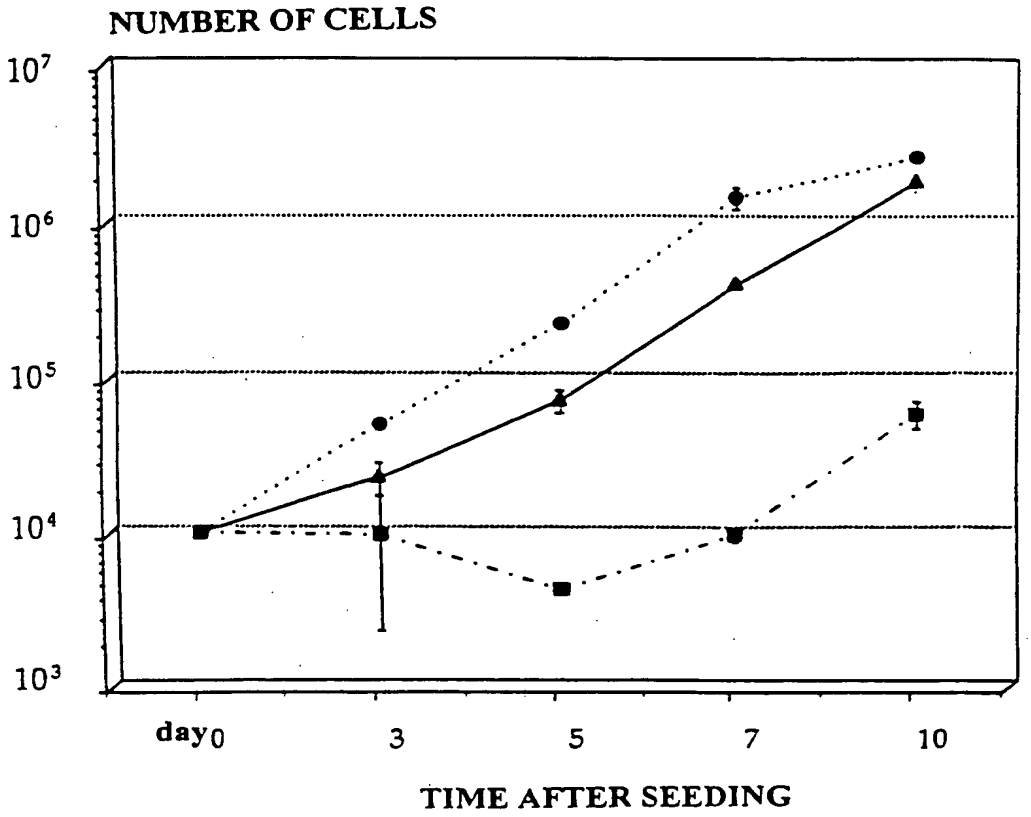
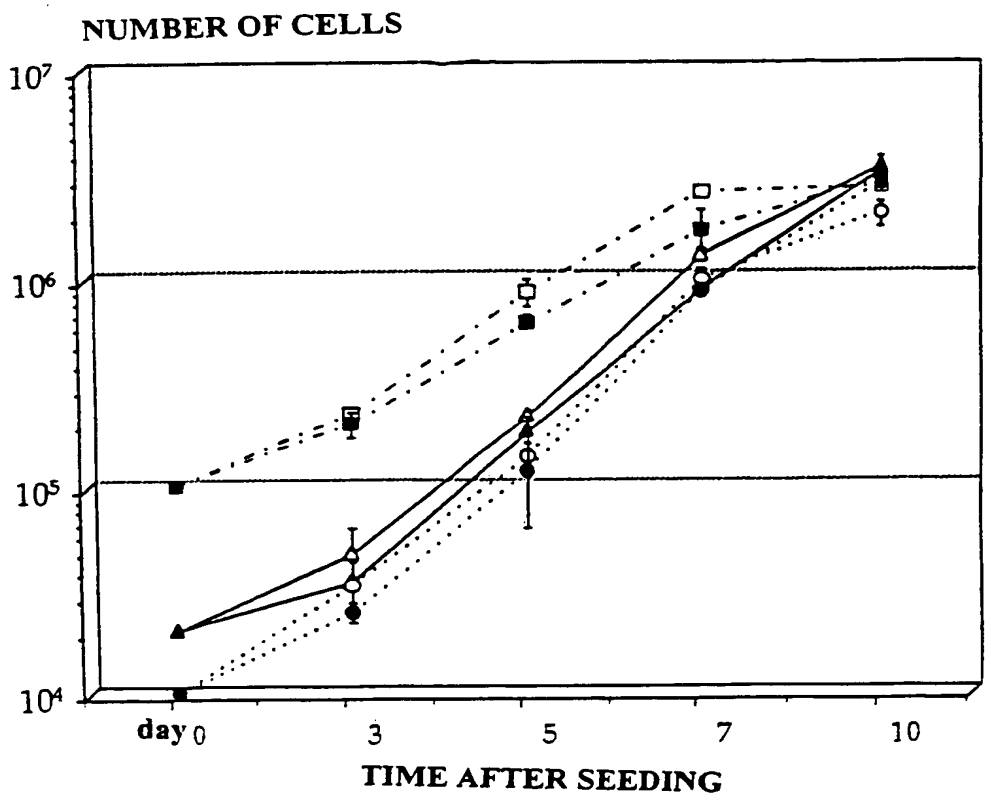
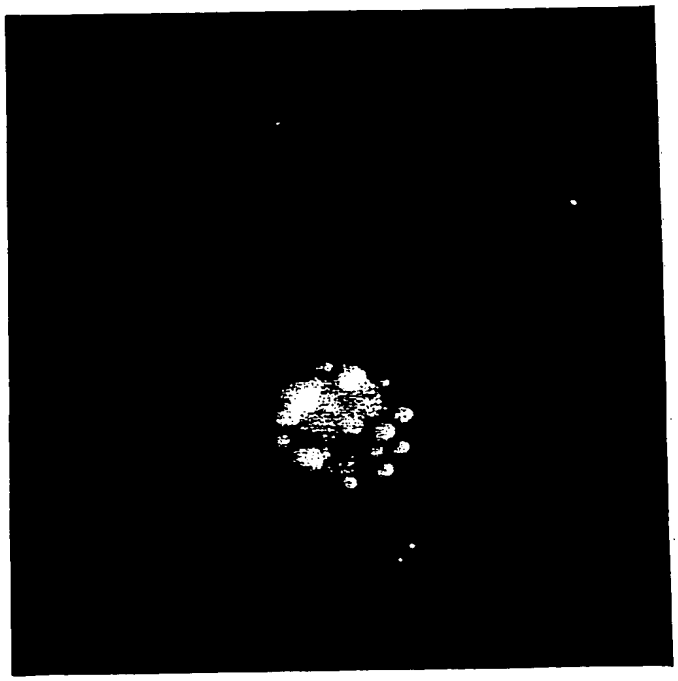


FIG. 17B





GFPkin17NLS-CT

FIG. 18B

GFPkin17ΔCT

FIG. 18A